AMENDMENT

IN THE SPECIFICATION

Please amend the specification as follows:

On page 13, line 17:

The invention concerns a method for the detection of a nucleic acid comprising the steps of producing a plurality of amplificates of a section of a nucleic acid with the aid of two primers, one of which can bind to a first binding sequence (A′) which is essentially complementary to a sequence A of a strand of the nucleic acid and of which the other can bind to a second binding sequence (C) which is located in the 3′ direction from A and does not overlap A, in the presence of a probe having a binding sequence D which can bind to a third sequence (B) located between the sequences A and C or to the complement (B′) thereof, wherein this probe contains a reporter group and a quencher group, using a polymerase having 5′ nuclease activity and detecting the nucleic acid by measuring a signal which is caused by release of the reporter group characterized in that the amplificates formed with the aid of the primers have a length of less than 100 nucleotides.

Page 19, line 32:

In the first essential step of the method according to the invention a segment of the nucleic acid to be detected is amplified. This segment is also referred to as an amplicon in the following. It is essential that this contains the sequence region between the outer ends of the sequences A′ and C or of the complement thereof (the primer binding regions) and contains the binding region E of the probe or of the complement thereof. According to the present invention the amplicon (preferably the total length of the sequences of the regions A, B and C) is preferably shorter than 100 nucleotides, particularly preferably shorter than 60 nucleotides, but preferably longer than 40 nucleotides. However, this does not mean that the total length of the amplificates cannot be larger e.g. when the primers have additional nucleotides that do not lie within the binding regions. Amplification methods are used which allow an amplification of the nucleic acid to be detected or the complement thereof and result in the formation of tripartite mini-nucleic acid amplification products (mini chain reaction (MCR)). In principle all nucleic acid amplification methods that are known in the prior art can be used for this. Target-specific nucleic acid amplification reactions are preferably used.

Theoretically exponentional target-specific nucleic acid amplification reactions are particularly preferably used in which an anti-parallel replication of the nucleic acid to be detected or of its complement is carried out e.g. elongation-based reactions such as the polymerase chain reaction (PCR for deoxyribonucleic acids, RT-PCR for ribonucleic acids). Thermocyclic exponential elongation-based nucleic acid amplification reactions are particularly preferred such as e.g. the polymerase chain reaction. The nucleic acids to be detected or complements thereof which are used for the amplification can be present in the form of single-stranded or double-stranded deoxyribonucleic acids or ribonucleic acids. The aim of the amplification reaction is to produce numerous amplificates of a segment of the nucleic acid to be detected. Hence an amplificate is understood as any molecular species produced by using sequence information of the nucleic acid. In particular the term refers to nucleic acids. The term "amplificate" includes single-stranded as well as double-stranded nucleic acids. In addition to the regions containing the sequence information of the underlying nucleic acid (amplicon), an amplificate can also contain additional regions which are not directly related to sequences of the nucleic acid to be amplified that are outside the ends of the primer binding sites which face away from another. Such sequences with a length of more than 15 nucleotides preferably do not occur on the nucleic acid to be detected or its complement and cannot hybridize with it by direct base pairing. Hence amplificates can either hybridize with the nucleic acid to be detected itself or with its complement. Amplificates are for example also products of an asymmetric amplification i.e. an amplification in which the two strands are formed in different amounts (e.g. by using different amounts of primers) or in which one of the two strands is subsequently destroyed (e.g. by RNase).

Page 24, line 1:

In the present invention the segment of the nucleic acid from which it is intended to produce a plurality of amplificates is selected such that it contains three regions A, B, and C. Regions A and C are regions selected such that one primer can use sequence A′ as the binding sequence and the complement of the region C′ can serve as the binding sequence for the other primer. A complement within the sense of the present invention is understood as a nucleic acid or nucleic acid sequence which is essentially complementary to a certain other nucleic acid e.g. a sequence region e.g. of an amplificate or of the nucleic acid to be detected.

Page 36, line 6:

The primers preferably bind to the binding sequences A′ or C as described above and the probe preferably binds to a region B located between the ends of the binding sequences A′ and C or to the complement thereof.

Page 48, line 2, abstract:

The invention concerns a method for the detection of a nucleic acid comprising the steps of producing a plurality of amplificates of a section of a nucleic acid having a length of less than 100 nucleotides with the aid of two primers, one of which can bind to a first binding sequence (A′) which is essentially complementary to a sequence A of a strand of the nucleic acid and the other can bind to a second binding sequence (C) which is located in the 3′ direction from (A) and does not overlap (A), which can bind in the presence of a probe with a binding sequence (D) which can bind to a third sequence (B) which is located between the sequences A and C or to the complement (B′) thereof, wherein this probe contains a reporter group and a quencher group using a polymerase having 5′ nuclease activity and detecting the nucleic acid by measuring a signal which is caused by the release of the reporter group.

IN THE CLAIMS

Please amend Claim 1 to read as follows:

1. (Five times amended) A method for the detection of a nucleic acid comprising:

   (a) producing a plurality of amplificates of a section of the nucleic acid by amplifying said section of nucleic acid with two primers, one of which binds to a first binding sequence A′ of one strand of the nucleic acid, wherein said binding sequence A′ is essentially complementary to a sequence A, located on the other strand of the nucleic acid, and the other primer binds to a second binding sequence C, which is located in the 3′ direction from A and does not overlap A, in the presence of a probe having a binding sequence D which binds to a third sequence B located between the sequences A and C or to the complement thereof, wherein the probe contains a reporter group and a quencher group, using a polymerase having 5′ nuclease activity; and

   (b) detecting the nucleic acid by measuring a signal which is caused by the release of the reporter group, wherein the amplificates have a length of 75 nucleotides or less, and the sequences located between the binding sequences A and C contains no nucleotides that do not belong to a sequence region E of the amplificate that is bound by binding sequence D of the probe.